10/580142 'AP9 Rec'd PCT/PTO 19 MAY 2006'

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PCT/CA2004/002001

SEQUENCE LISTING

<11	10>	Brur Raud Gall	ham, loni) icha	Rob ciene	e, Au	ısra	ted									
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190

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- Ser Leu Leu Thr Ser Ala Ala Pro Leu Asp Gln Glu Gly Ser Leu Tyr 225 230 235 240
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- Leu Ser Ser Lys Ser Asn Pro Glu Val Ala Leu Ala Ala Ala Gln Thr 260 265 270
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Ser Lys Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys
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Leu Glu Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala 420 425 430

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Ser Lys Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala 450 455 460

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Asp Ala Glu Asn Pro Leu Pro Ser Pro Ser Ser Ser Tyr Leu Arg Tyr 500 505 510

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tac Tyr	cgt Arg 130	ctg Leu	gcc Ala	tgt Cys	atg Met	aaa Lys 135	aac Asn	agt Ser	aaa Lys	gta Val	agt Ser 140	gac Asp	tac Tyr	ctc Leu	tat Tyr	432
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cgt Arg	att Ile	cta Leu	act Thr	tca Ser 405	caa Gln	aaa Lys	acc Thr	cct Pro	cta Leu 410	gca Ala	gct Ala	aaa Lys	gct Ala	att Ile 415	gct Ala		1248
ttt Phe	tta Leu	tca Ser	gta Val 420	aca Thr	gct Ala	cat His	cct Pro	cag Gln 425	gca Ala	ctt Leu	tct Ser	tta Leu	gtc Val 430	tcg Ser	aaa Lys		1296
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caa Gln : 465	Tyr	Ala	Glu	Gln	Leu 470	Ile	Gly	Asp	Thr	Ile 475	Leu	Phe	Thr	Asp	Glu 480		1440
gag a Glu i	Asn	Pro	Leu	Pro 485	Ser	Pro	His	Ser	Ser 490	Tyr	Leu	Arg	Tyr	Gln 495	Val		1488
tcc (Ser 1	Pro	Glu	Thr 500	Arg	Ser	Gln	Leu	Met 505	Leu	Thr	Ile	Leu	Glu 510	Thr	Leu		1536
gtt t Val s	Ser	Ser 515	Lys	Thr	Asp	Glu	Asp 520	Ile	Arg	Val	Phe	Leu 525	Ser	Leu	Met		1584
	530	Thr	His	Tyr	Lys	Asn 535	Ile	Pro	Ile	Leu	Ser 540	Gly	Leu	Leu	Met		1632
aga a Arg I 545	Ile	Val	Glu	Arg	gct Ala 550	cgg Arg	tac Tyr	caa Gln	gct Ala	tac Tyr 555	gta Val	gaa Glu	caa Gln	aaa Lys	ctc Leu 560		1680
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Tyr Leu Gln Gln Ser Leu Phe Ser Glu Asp Ala Tyr Val Arg Lys Ser 50 55 60

Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu Asp Leu 65 70 75 80

Leu Ser Glu Ser Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu Leu Ile 85 90 95

Leu Asn Ala Gly Asn Gln Leu Gly Lys Thr Ser Asp Arg Leu Leu 100 105 110

Phe Lys Gly Leu Thr Ala Pro His Pro Ile Ile Arg Leu Glu Ala Ala 115 120 125

Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr 130 135 140

Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Val His Arg 165 170 175

Leu Leu Ser Ser Pro Asn Ser Leu Thr Arg Asn Tyr Met Ala Tyr Leu 180 185 190

Ile Gly Glu Tyr Gln Gln Arg Arg Phe Leu Pro Thr Leu Arg Ser Leu 195 200 205

Leu Thr Ser Ala Ala Pro Leu Asp Gln Glu Gly Ser Leu Tyr Ala Ile 210 215 220

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- Glu Glu Ile Lys Leu Asn Ala Ala Leu Ala Leu Val His Leu Gly Ser 305 310 315 320
- Val Asn His Leu Val Leu Ser Tyr Leu Thr Glu Phe Leu Glu Asn Lys
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 330
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- Ile Leu His Arg Ile Phe Leu Pro Thr His Ser Ile Gly Lys Ala Thr 340 345 350
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ATa	це ц 450	Tyr	rnr	мет	TNT	G1n 455	Asp	Pro	G1u	Гуз	Lys 460	Ala	Leu	Leu	Tyr				
Gln 465	Tyr	Ala	Glu	Gln	Leu 470	Ile	Gly	Asp	Thr	Ile 475		Phe	Thr	Asp	Glu 480				
Glu	Asn	Pro	Leu	Pro 485	Ser	Pro	His	Ser	Ser 490	Tyr	Leu	Arg	Tyr	Gln 495	Val				
Ser	Pro	Glu	Thr 500	Arg	Ser	Gln	Leu	Met 505	Leu	Thr	Ile	Leu	Glu 510	Thr	Leu			,	
Val	Ser	Ser 515	Lys	Thr	Asp	Glu	Asp 520	Ile	Arg	Val	Phe	Leu 525	Ser	Leu	Met	•			
Lys	Lys 530	Thr	His	Tyr	Lys	Asn 535	Ile	Pro	Ile	Leu	Ser 540	Gly	Leu	Leu	Met				
Arg	Ile	Val	Glu	Arg	Ala	Arg	Tyr	Gln	Ala	Tyr	Val	Glu	Gln	Lys	Leu	•	-		
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Ile	Ser	Glu	Glu	Asp 565															
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gaa gaa att aga Glu Glu Ile Arq 305	ctg aat act Leu Asn Thr 310	gct tta gca Ala Leu Ala	ctt gtt cat cas Leu Val His Glr 315	a ggg tgt 960 n Gly Cys 320	D
aca gat cct cad Thr Asp Pro Gli	gtc ctc cac Val Leu His 325	tat cta aca Tyr Leu Thr 330	gaa atc tta gaa Glu Ile Leu Glu	a agt aaa 1000 1 Ser Lys 335	В
gtt ctc cat cgc Val Leu His Arg 340	J Ile Phe Leu	cct act cac Pro Thr His 345	tcg aca gga aaa Ser Thr Gly Lys 350	Ala Ile	6
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	Thr Ala His		ctt tct tta gto Leu Ser Leu Val 430	l Ser Lys	6
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Ser Phe lie Tyr Lys Leu Pro Giu Glu Ile Gin Asn Leu Ala Ala Thr 145 150 155 160

- Ile Phe Leu Glu Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile His His 165 170 175
- Leu Leu Ser Ser Pro Asn Asn Leu Thr Arg Asn Tyr Val Ala Tyr Leu 180 185 190
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- Leu Thr Ser Ala Ser Pro Leu Asp Gln Glu Gly Ala Leu Tyr Ala Leu 210 215 220
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375 370 380 Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr Leu Glu 385 390 395 400 Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala Ile Ala 405 410 415 Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys 420 425 Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu 435 . 440 Ala Leu Tyr Thr Met Thr Lys Asp Pro Glu Lys Lys Ala Val Leu Tyr 460 450 455 Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr Asp Ala Glu Asn Pro Leu Pro Ser Pro Ser Ser Ser Tyr Leu Arg Tyr Gln Val 490 495 Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu Thr Leu 500 505 Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met . 515 520 525 Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met 530 535 540 Arg Ile Val Glu 545 <210> 9 <211> 41 <212> DNA <213> Chlamydia trachomatis <400> 9

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